

=====

Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2010; month=1; day=29; hr=12; min=54; sec=12; ms=945;]

=====

Application No: 10568422 Version No: 2.0

Input Set:

Output Set:

Started: 2010-01-15 10:28:01.076
Finished: 2010-01-15 10:28:09.492
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 416 ms
Total Warnings: 2
Total Errors: 23
No. of SeqIDs Defined: 93
Actual SeqID Count: 93

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (16)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (30)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (33)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (45)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (46)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (56)

Input Set:

Output Set:

Started: 2010-01-15 10:28:01.076
Finished: 2010-01-15 10:28:09.492
Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 416 ms
Total Warnings: 2
Total Errors: 23
No. of SeqIDs Defined: 93
Actual SeqID Count: 93

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (81)
E 321	No. of Bases conflict, this line has no nucleotides SEQID (91)
W 213	Artificial or Unknown found in <213> in SEQ ID (92)
W 213	Artificial or Unknown found in <213> in SEQ ID (93)

SEQUENCE LISTING

<110> Telford, John L.
Grandi, Guido
Margarit Y Ros, Immaculada
Maione, Domenico

<120> Immunogenic Compositions for Streptococcus agalactiae

<130> PP20665.0003

<140> 10568422
<141> 2010-01-15
002441.00189

<150> PCT/US04/030032
<151> 2004-09-15

<150> US 60/548,789
<151> 2004-02-28

<150> PCT/US03/29167
<151> 2003-09-15

<160> 93

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1662
<212> DNA
<213> Streptococcus agalactiae

<400> 1
atgaaattat cgaagaagtt attgttttcg gctgctgttt taacaatggt ggcggggtca 60
actgttgaac cagtagctca gtttgcgact ggaatgagta ttgtaagagc tgcagaagtg 120
tcacaagaac gccagcga aacaacagta aatatctata aattacaagc tgatagttat 180
aaatcgga aaatcttctaa tgggtggtatc gagaataaag acggcgaagt aatatctaac 240
tatgctaaac ttggtgacaa tgtaaaagggt ttgcaagggtg tacagtttaa acgttataaa 300
gtcaagacgg atatttctgt tgatgaattg aaaaaattga caacagttga agcagcagat 360
gcaaaagttg gaacgattct tgaagaagggt gtcagctctac ctcaaaaaac taatgctcaa 420
gggttggtcg tcgatgctct ggattcaaaa agtaatgtga gatacttgta tgtagaagat 480
ttaaagaatt caccttcaaa cattacaaa gcttatgctg taccgtttgt gttggaatta 540
ccagttgcta actctacagg tacagggtttc ctttctgaaa ttaatattta ccctaaaaac 600
gttgtaactg atgaaccaa aacagataaa gatgttaaaa aattaggtca ggacgatgca 660
gggtatacga ttggtgaaga attcaaattg ttcttgaaat ctacaatccc tgccaattta 720
gggtgactatg aaaaatttga aattactgat aaatttgcag atggcttgac ttataaatct 780
gttggaaaaa tcaagattgg ttcgaaaaca ctgaatagag atgagcacta cactattgat 840
gaaccaacag ttgataacca aaatacatta aaaattacgt ttaaaccaga gaaatttaaa 900
gaaattgctg agctacttaa aggaatgacc cttgttaaaa atcaagatgc tcttgataaa 960
gctactgcaa atacagatga tgcggcattt ttggaaattc cagttgcatc aactattaat 1020
gaaaaagcag ttttaggaaa agcaattgaa aatacttttg aacttcaata tgaccatact 1080
cctgataaag ctgacaatcc aaaccatct aatcctccaa gaaaaccaga agttcatact 1140
gggtgggaaac gatttgtaaa gaaagactca acagaaacac aaacactagg tgggtgctgag 1200
tttgatttgt tggcttctga tgggacagca gtaaaatgga cagatgctct tattaagcgc 1260

```

aataactaata aaaactatat tgctggagaa gctgttactg ggcaaccaat caaattgaaa 1320
tcacatacag acggtacgtt tgagattaaa ggtttggctt atgcagttga tgcgaatgca 1380
gaggggtacag cagtaactta caaattaaaa gaaacaaaag caccagaagg ttatgtaatc 1440
cctgataaaag aaatcgagtt tacagtatca caaacatctt ataatacaaa accaactgac 1500
atcacgggttg atagtgtcga tgcaacacct gatacaatta aaaacaacaa acgtccttca 1560
atccctaata ctgggtgggtat tgggtacggct atctttgtcg ctatcgggtgc tgcgggtgatg 1620
gcttttgcgtg ttaaggggat gaagcgtcgt acaaaagata ac 1662

```

<210> 2

<211> 554

<212> PRT

<213> Streptococcus agalactiae

<400> 2

```

Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
  1             5             10             15
Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
          20             25             30
Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
          35             40             45
Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
  50             55             60
Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
  65             70             75             80
Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
          85             90             95
Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
          100            105            110
Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
          115            120            125
Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
          130            135            140
Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
          145            150            155            160
Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
          165            170            175
Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
          180            185            190
Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
          195            200            205
Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
          210            215            220
Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
          225            230            235            240
Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
          245            250            255
Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
          260            265            270
Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
          275            280            285
Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu
          290            295            300
Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
          305            310            315            320
Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
          325            330            335
Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr

```

	340		345		350										
Phe	Glu	Leu	Gln	Tyr	Asp	His	Thr	Pro	Asp	Lys	Ala	Asp	Asn	Pro	Lys
	355						360					365			
Pro	Ser	Asn	Pro	Pro	Arg	Lys	Pro	Glu	Val	His	Thr	Gly	Gly	Lys	Arg
	370					375					380				
Phe	Val	Lys	Lys	Asp	Ser	Thr	Glu	Thr	Gln	Thr	Leu	Gly	Gly	Ala	Glu
385					390					395					400
Phe	Asp	Leu	Leu	Ala	Ser	Asp	Gly	Thr	Ala	Val	Lys	Trp	Thr	Asp	Ala
			405						410					415	
Leu	Ile	Lys	Ala	Asn	Thr	Asn	Lys	Asn	Tyr	Ile	Ala	Gly	Glu	Ala	Val
			420					425					430		
Thr	Gly	Gln	Pro	Ile	Lys	Leu	Lys	Ser	His	Thr	Asp	Gly	Thr	Phe	Glu
		435					440					445			
Ile	Lys	Gly	Leu	Ala	Tyr	Ala	Val	Asp	Ala	Asn	Ala	Glu	Gly	Thr	Ala
	450					455					460				

Val	Thr	Tyr	Lys	Leu	Lys	Glu	Thr	Lys	Ala	Pro	Glu	Gly	Tyr	Val	Ile
465					470					475					480
Pro	Asp	Lys	Glu	Ile	Glu	Phe	Thr	Val	Ser	Gln	Thr	Ser	Tyr	Asn	Thr
				485					490					495	

Lys	Pro	Thr	Asp	Ile	Thr	Val	Asp	Ser	Ala	Asp	Ala	Thr	Pro	Asp	Thr
			500					505					510		
Ile	Lys	Asn	Asn	Lys	Arg	Pro	Ser	Ile	Pro	Asn	Thr	Gly	Gly	Ile	Gly
		515					520					525			
Thr	Ala	Ile	Phe	Val	Ala	Ile	Gly	Ala	Ala	Val	Met	Ala	Phe	Ala	Val
	530					535					540				
Lys	Gly	Met	Lys	Arg	Arg	Thr	Lys	Asp	Asn						
545					550										

<210> 3

<211> 517

<212> PRT

<213> Streptococcus agalactiae

<400> 3

Ala	Glu	Val	Ser	Gln	Glu	Arg	Pro	Ala	Lys	Thr	Thr	Val	Asn	Ile	Tyr
1				5					10					15	
Lys	Leu	Gln	Ala	Asp	Ser	Tyr	Lys	Ser	Glu	Ile	Thr	Ser	Asn	Gly	Gly
		20						25					30		
Ile	Glu	Asn	Lys	Asp	Gly	Glu	Val	Ile	Ser	Asn	Tyr	Ala	Lys	Leu	Gly
	35					40					45				
Asp	Asn	Val	Lys	Gly	Leu	Gln	Gly	Val	Gln	Phe	Lys	Arg	Tyr	Lys	Val
	50					55					60				
Lys	Thr	Asp	Ile	Ser	Val	Asp	Glu	Leu	Lys	Lys	Leu	Thr	Thr	Val	Glu
65					70					75					80
Ala	Ala	Asp	Ala	Lys	Val	Gly	Thr	Ile	Leu	Glu	Glu	Gly	Val	Ser	Leu
				85					90					95	
Pro	Gln	Lys	Thr	Asn	Ala	Gln	Gly	Leu	Val	Val	Asp	Ala	Leu	Asp	Ser
		100						105					110		
Lys	Ser	Asn	Val	Arg	Tyr	Leu	Tyr	Val	Glu	Asp	Leu	Lys	Asn	Ser	Pro
		115					120					125			
Ser	Asn	Ile	Thr	Lys	Ala	Tyr	Ala	Val	Pro	Phe	Val	Leu	Glu	Leu	Pro
	130					135					140				
Val	Ala	Asn	Ser	Thr	Gly	Thr	Gly	Phe	Leu	Ser	Glu	Ile	Asn	Ile	Tyr
145					150					155					160
Pro	Lys	Asn	Val	Val	Thr	Asp	Glu	Pro	Lys	Thr	Asp	Lys	Asp	Val	Lys

				165					170					175			
Lys	Leu	Gly	Gln	Asp	Asp	Ala	Gly	Tyr	Thr	Ile	Gly	Glu	Glu	Phe	Lys		
			180					185					190				
Trp	Phe	Leu	Lys	Ser	Thr	Ile	Pro	Ala	Asn	Leu	Gly	Asp	Tyr	Glu	Lys		
		195					200					205					
Phe	Glu	Ile	Thr	Asp	Lys	Phe	Ala	Asp	Gly	Leu	Thr	Tyr	Lys	Ser	Val		
	210					215					220						
Gly	Lys	Ile	Lys	Ile	Gly	Ser	Lys	Thr	Leu	Asn	Arg	Asp	Glu	His	Tyr		
225				230					235						240		
Thr	Ile	Asp	Glu	Pro	Thr	Val	Asp	Asn	Gln	Asn	Thr	Leu	Lys	Ile	Thr		
			245					250						255			
Phe	Lys	Pro	Glu	Lys	Phe	Lys	Glu	Ile	Ala	Glu	Leu	Leu	Lys	Gly	Met		
		260						265					270				
Thr	Leu	Val	Lys	Asn	Gln	Asp	Ala	Leu	Asp	Lys	Ala	Thr	Ala	Asn	Thr		
	275				280						285						
Asp	Asp	Ala	Ala	Phe	Leu	Glu	Ile	Pro	Val	Ala	Ser	Thr	Ile	Asn	Glu		
	290				295				300								
Lys	Ala	Val	Leu	Gly	Lys	Ala	Ile	Glu	Asn	Thr	Phe	Glu	Leu	Gln	Tyr		
305				310					315						320		
Asp	His	Thr	Pro	Asp	Lys	Ala	Asp	Asn	Pro	Lys	Pro	Ser	Asn	Pro	Pro		
			325					330					335				
Arg	Lys	Pro	Glu	Val	His	Thr	Gly	Gly	Lys	Arg	Phe	Val	Lys	Lys	Asp		
	340						345					350					
Ser	Thr	Glu	Thr	Gln	Thr	Leu	Gly	Gly	Ala	Glu	Phe	Asp	Leu	Leu	Ala		
	355			360				365									
Ser	Asp	Gly	Thr	Ala	Val	Lys	Trp	Thr	Asp	Ala	Leu	Ile	Lys	Ala	Asn		
	370			375				380									
Thr	Asn	Lys	Asn	Tyr	Ile	Ala	Gly	Glu	Ala	Val	Thr	Gly	Gln	Pro	Ile		
385				390				395						400			
Lys	Leu	Lys	Ser	His	Thr	Asp	Gly	Thr	Phe	Glu	Ile	Lys	Gly	Leu	Ala		
			405					410					415				
Tyr	Ala	Val	Asp	Ala	Asn	Ala	Glu	Gly	Thr	Ala	Val	Thr	Tyr	Lys	Leu		
	420						425					430					
Lys	Glu	Thr	Lys	Ala	Pro	Glu	Gly	Tyr	Val	Ile	Pro	Asp	Lys	Glu	Ile		
	435					440					445						
Glu	Phe	Thr	Val	Ser	Gln	Thr	Ser	Tyr	Asn	Thr	Lys	Pro	Thr	Asp	Ile		
	450				455						460						
Thr	Val	Asp	Ser	Ala	Asp	Ala	Thr	Pro	Asp	Thr	Ile	Lys	Asn	Asn	Lys		
465				470					475					480			
Arg	Pro	Ser	Ile	Pro	Asn	Thr	Gly	Gly	Ile	Gly	Thr	Ala	Ile	Phe	Val		
			485					490					495				
Ala	Ile	Gly	Ala	Ala	Val	Met	Ala	Phe	Ala	Val	Lys	Gly	Met	Lys	Arg		
	500					505					510						
Arg	Thr	Lys	Asp	Asn													
	515																

<210> 4

<211> 525

<212> PRT

<213> Streptococcus agalactiae

<400> 4

Met	Lys	Leu	Ser	Lys	Lys	Leu	Leu	Phe	Ser	Ala	Ala	Val	Leu	Thr	Met
1				5				10					15		
Val	Ala	Gly	Ser	Thr	Val	Glu	Pro	Val	Ala	Gln	Phe	Ala	Thr	Gly	Met
	20						25					30			
Ser	Ile	Val	Arg	Ala	Ala	Glu	Val	Ser	Gln	Glu	Arg	Pro	Ala	Lys	Thr

35	40	45
Thr Val Asn Ile Tyr Lys	Leu Gln Ala Asp Ser Tyr	Lys Ser Glu Ile
50	55	60
Thr Ser Asn Gly Gly Ile	Glu Asn Lys Asp Gly Glu	Val Ile Ser Asn
65	70	75
Tyr Ala Lys Leu Gly Asp	Asn Val Lys Gly Leu	Gln Gly Val Gln Phe
85	90	95
Lys Arg Tyr Lys Val Lys	Thr Asp Ile Ser Val	Asp Glu Leu Lys Lys
100	105	110
Leu Thr Thr Val Glu Ala	Ala Asp Ala Lys Val	Gly Thr Ile Leu Glu
115	120	125
Glu Gly Val Ser Leu Pro	Gln Lys Thr Asn Ala	Gln Gly Leu Val Val
130	135	140
Asp Ala Leu Asp Ser Lys	Ser Asn Val Arg Tyr	Leu Tyr Val Glu Asp
145	150	155
Leu Lys Asn Ser Pro Ser	Asn Ile Thr Lys Ala	Tyr Ala Val Pro Phe
165	170	175
Val Leu Glu Leu Pro Val	Ala Asn Ser Thr Gly	Thr Gly Phe Leu Ser
180	185	190
Glu Ile Asn Ile Tyr Pro	Lys Asn Val Val Thr	Asp Glu Pro Lys Thr
195	200	205
Asp Lys Asp Val Lys Lys	Leu Gly Gln Asp Asp	Ala Gly Tyr Thr Ile
210	215	220
Gly Glu Glu Phe Lys Trp	Phe Leu Lys Ser Thr	Ile Pro Ala Asn Leu
225	230	235
Gly Asp Tyr Glu Lys Phe	Glu Ile Thr Asp Lys	Phe Ala Asp Gly Leu
245	250	255
Thr Tyr Lys Ser Val Gly	Lys Ile Lys Ile Gly	Ser Lys Thr Leu Asn
260	265	270
Arg Asp Glu His Tyr Thr	Ile Asp Glu Pro Thr	Val Asp Asn Gln Asn
275	280	285
Thr Leu Lys Ile Thr Phe	Lys Pro Glu Lys Phe	Lys Glu Ile Ala Glu
290	295	300
Leu Leu Lys Gly Met Thr	Leu Val Lys Asn Gln	Asp Ala Leu Asp Lys
305	310	315
Ala Thr Ala Asn Thr Asp	Asp Ala Ala Phe Leu	Glu Ile Pro Val Ala
325	330	335
Ser Thr Ile Asn Glu Lys	Ala Val Leu Gly Lys	Ala Ile Glu Asn Thr
340	345	350
Phe Glu Leu Gln Tyr Asp	His Thr Pro Asp Lys	Ala Asp Asn Pro Lys
355	360	365
Pro Ser Asn Pro Pro Arg	Lys Pro Glu Val His	Thr Gly Gly Lys Arg
370	375	380
Phe Val Lys Lys Asp Ser	Thr Glu Thr Gln Thr	Leu Gly Gly Ala Glu
385	390	395
Phe Asp Leu Leu Ala Ser	Asp Gly Thr Ala Val	Lys Trp Thr Asp Ala
405	410	415
Leu Ile Lys Ala Asn Thr	Asn Lys Asn Tyr Ile	Ala Gly Glu Ala Val
420	425	430
Thr Gly Gln Pro Ile Lys	Leu Lys Ser His Thr	Asp Gly Thr Phe Glu
435	440	445
Ile Lys Gly Leu Ala Tyr	Ala Val Asp Ala Asn	Ala Glu Gly Thr Ala
450	455	460
Val Thr Tyr Lys Leu Lys	Glu Thr Lys Ala Pro	Glu Gly Tyr Val Ile
465	470	475
Pro Asp Lys Glu Ile Glu	Phe Thr Val Ser Gln	Thr Ser Tyr Asn Thr
485	490	495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500 505 510
Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly
515 520 525

<210> 5
<211> 5
<212> PRT
<213> Streptococcus agalactiae

<400> 5
Ile Pro Asn Thr Gly
1 5

<210> 6
<211> 520
<212> PRT
<213> Streptococcus agalactiae

<400> 6
Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
1 5 10 15
Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
20 25 30
Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
35 40 45
Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
50 55 60
Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65 70 75 80
Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85 90 95
Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
100 105 110
Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
115 120 125
Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
130 135 140
Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
145 150 155 160
Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
165 170 175
Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
180 185 190
Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
195 200 205
Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
210 215 220
Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
225 230 235 240
Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
245 250 255
Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
260 265 270
Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
275 280 285
Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu

290						295						300					
Leu	Leu	Lys	Gly	Met	Thr	Leu	Val	Lys	Asn	Gln	Asp	Ala	Leu	Asp	Lys		
305						310				315					320		
Ala	Thr	Ala	Asn	Thr	Asp	Asp	Ala	Ala	Phe	Leu	Glu	Ile	Pro	Val	Ala		
				325					330					335			
Ser	Thr	Ile	Asn	Glu	Lys	Ala	Val	Leu	Gly	Lys	Ala	Ile	Glu	Asn	Thr		
			340						345								